

B. Hutson

Re-run



RAW SEQUENCE LISTING

DATE: 11/19/2002

PATENT APPLICATION: US/09/701,586C

TIME: 10:23:20

Input Set : N:\Cr4\11132002\I701586C.raw

Output Set: N:\CRF4\11192002\I701586C.raw

C--> 1 <110> APPLICANT: Kock, Michael
2 Hoeger, Thomas
3 Kroeger, Burkhard
4 Otterbach, Bernd
5 Lubisch, Wilfried
6 Lemaire, Hans-Georg
7 <120> TITLE OF INVENTION: Poly (ADP-ribose) polymerase-gene
8 <130> FILE REFERENCE: 0050/49100
9 <140> CURRENT APPLICATION NUMBER: US/09/701,586C
10 <141> CURRENT FILING DATE: 2000-11-30
11 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03889
12 <151> PRIOR FILING DATE: 1999-06-04
13 <160> NUMBER OF SEQ ID NOS: 33
14 <170> SOFTWARE: PatentIn/WordPerfect
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17 <211> LENGTH: 1843
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (3)...(1715)
23 <223> OTHER INFORMATION: product is Poly ADP Ribose Polymerase; from brain tissue
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28 gca tta aat gaa agc aaa aga gtt aat aat ggc aac acg gct cca gaa 95
29 Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu
30 20 25 30
31 gac tct tcc cct gcc aag aaa act cgt aga tgc cag aga cag gag tcg 143
32 Asp Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser
33 35 40 45
34 aaa aag atg cct gtg gct gga gga aaa gct aat aag gac agg aca gaa 191
35 Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu
36 50 55 60
37 gac aag caa gat gaa tct gtg aag gcc ttg ctg tta aag ggc aaa gct 239
38 Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala
39 65 70 75
40 cct gtg gac cca gag tgt aca gcc aag gtg ggg aag gct cat gtg tat 287
41 Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr
42 80 85 90 95
43 tgt gaa gga aat gat gtc tat gat gtc atg cta aat cag acc aat ctc 335
44 Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu

ENTERED

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Input Set : N:\Crf4\11132002\I701586C.raw

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48				115					120					125			
49	gcc	cag	agg	aac	ttc	agt	gtt	tgg	atg	aga	tgg	ggc	cga	gtt	ggg	aaa	431
50	Ala	Gln	Arg	Asn	Phe	Ser	Val	Trp	Met	Arg	Trp	Gly	Arg	Val	Gly	Lys	
51				130					135					140			
52	atg	gga	cag	cac	agc	ctg	gtg	gct	tgt	tca	ggc	aat	ctc	aac	aag	gcc	479
53	Met	Gly	Gln	His	Ser	Leu	Val	Ala	Cys	Ser	Gly	Asn	Leu	Asn	Lys	Ala	
54				145					150					155			
55	aag	gaa	atc	ttt	cag	aag	aaa	ttc	ctt	gac	aaa	acg	aaa	aac	aat	tgg	527
56	Lys	Glu	Ile	Phe	Gln	Lys	Lys	Phe	Leu	Asp	Lys	Thr	Lys	Asn	Asn	Trp	
57	160								165					170			
58	gaa	gat	cga	gaa	aag	ttt	gag	aag	gtg	cct	gga	aaa	tat	gat	atg	cta	575
59	Glu	Asp	Arg	Glu	Lys	Phe	Glu	Lys	Val	Pro	Gly	Lys	Tyr	Asp	Met	Leu	
60					180					185					190		
61	cag	atg	gac	tat	gcc	acc	aat	act	cag	gat	gaa	gag	gaa	aca	aag	aaa	623
62	Gln	Met	Asp	Tyr	Ala	Thr	Asn	Thr	Gln	Asp	Glu	Glu	Glu	Thr	Lys	Lys	
63				195					200					205			
64	gag	gaa	tct	ctt	aaa	tct	ccc	ttg	aag	cca	gag	tca	cag	cta	gat	ctt	671
65	Glu	Glu	Ser	Leu	Lys	Ser	Pro	Leu	Lys	Pro	Glu	Ser	Gln	Leu	Asp	Leu	
66				210					215					220			
67	cgg	gta	cag	gag	tta	ata	aag	ttg	atc	tgt	aat	gtt	cag	gcc	atg	gaa	719
68	Arg	Val	Gln	Glu	Leu	Ile	Lys	Leu	Ile	Cys	Asn	Val	Gln	Ala	Met	Glu	
69				225					230					235			
70	gaa	atg	atg	atg	gaa	atg	aag	tat	aat	acc	aag	aaa	gcc	cca	ctt	ggg	767
71	Glu	Met	Met	Met	Glu	Met	Lys	Tyr	Asn	Thr	Lys	Lys	Ala	Pro	Leu	Gly	
72	240								245					250		255	
73	aag	ctg	aca	gtg	gca	caa	atc	aag	gca	ggt	tac	cag	tct	ctt	aag	aag	815
74	Lys	Leu	Thr	Val	Ala	Gln	Ile	Lys	Ala	Gly	Tyr	Gln	Ser	Leu	Lys	Lys	
75					260					265					270		
76	att	gag	gat	tgt	att	cgg	gct	ggc	cag	cat	gga	cga	gct	ctc	atg	gaa	863
77	Ile	Glu	Asp	Cys	Ile	Arg	Ala	Gly	Gln	His	Gly	Arg	Ala	Leu	Met	Glu	
78				275					280					285			
79	gca	tgc	aat	gaa	ttc	tac	acc	agg	att	ccg	cat	gac	ttt	gga	ctc	cgt	911
80	Ala	Cys	Asn	Glu	Phe	Tyr	Thr	Arg	Ile	Pro	His	Asp	Phe	Gly	Leu	Arg	
81				290					295					300			
82	act	cct	cca	cta	atc	cgg	aca	cag	aag	gaa	ctg	tca	gaa	aaa	ata	caa	959
83	Thr	Pro	Pro	Leu	Ile	Arg	Thr	Gln	Lys	Glu	Leu	Ser	Glu	Lys	Ile	Gln	
84				305					310					315			
85	tta	cta	gag	gct	ttg	gga	gac	att	gaa	att	gct	att	aag	ctg	gtg	aaa	1007
86	Leu	Leu	Glu	Ala	Leu	Gly	Asp	Ile	Glu	Ile	Ala	Ile	Lys	Leu	Val	Lys	
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88	aca	gag	cta	caa	agc	cca	gaa	cac	cca	ttg	gac	caa	cac	tat	aga	aac	1055
89	Thr	Glu	Leu	Gln	Ser	Pro	Glu	His	Pro	Leu	Asp	Gln	His	Tyr	Arg	Asn	
90					340					345				350			
91	cta	cat	tgt	gcc	ttg	cgc	ccc	ctt	gac	cat	gaa	agt	tac	gag	ttc	aaa	1103
92	Leu	His	Cys	Ala	Leu	Arg	Pro	Leu	Asp	His	Glu	Ser	Tyr	Glu	Phe	Lys	
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Input Set : N:\Crf4\11132002\I701586C.raw

Output Set: N:\CRF4\11192002\I701586C.raw

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95      Val Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp
96              370                      375                      380
97      tat acc atg acc ttg ctg gat ttg ttt gaa gtg gag aag gat ggt gag      1199
98      Tyr Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu
99              385                      390                      395
100     aaa gaa gcc ttc aga gag gac ctt cat aac agg atg ctt cta tgg cat      1247
101     Lys Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His
102     400                      405                      410                      415
103     ggt tcc agg atg agt aac tgg gtg gga atc ttg agc cat ggg ctt cga      1295
104     Gly Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg
105              420                      425                      430
106     att gcc cca cct gaa gct ccc atc aca ggt tac atg ttt ggg aaa gga      1343
107     Ile Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly
108              435                      440                      445
109     atc tac ttt gct gac atg tct tcc aag agt gcc aat tac tgc ttt gcc      1391
110     Ile Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala
111              450                      455                      460
112     tct cgc cta aag aat aca gga ctg ctg ctc tta tca gag gta gct cta      1439
113     Ser Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu
114     465                      470                      475
115     ggt cag tgt aat gaa cta cta gag gcc aat cct aag gcc gaa gga ttg      1487
116     Gly Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu
117     480                      485                      490                      495
118     ctt caa ggt aaa cat agc acc aag ggg ctg ggc aag atg gct ccc agt      1535
119     Leu Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser
120              500                      505                      510
121     tct gcc cac ttc gtc acc ctg aat ggg agt aca gtg cca tta gga cca      1583
122     Ser Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro
123              515                      520                      525
124     gca agt gac aca gga att ctg aat cca gat ggt tat acc ctc aac tac      1631
125     Ala Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr
126     530                      535                      540
127     aat gaa tat att gta tat aac ccc aac cag gtc cgt atg cgg tac ctt      1679
128     Asn Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu
129     545                      550                      555
130     tta aag gtt cag ttt aat ttc ctt cag ctg tgg tga atgttgatat      1725
131     Leu Lys Val Gln Phe Asn Phe Leu Gln Leu Trp
132     560                      565                      570
133     taaataaacc agagatctga tcttcaagca agaaaataag cagtgttgta cttgtgaatt      1785
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138 <212> TYPE: PRT
139 <213> ORGANISM: Homo sapiens
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Input Set : N:\Crf4\11132002\I701586C.raw

Output Set: N:\CRF4\11192002\I701586C.raw

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148		50				55						60				
149	Lys	Gln	Asp	Glu	Ser	Val	Lys	Ala	Leu	Leu	Leu	Lys	Gly	Lys	Ala	Pro
150	65					70					75					80
151	Val	Asp	Pro	Glu	Cys	Thr	Ala	Lys	Val	Gly	Lys	Ala	His	Val	Tyr	Cys
152					85					90					95	
153	Glu	Gly	Asn	Asp	Val	Tyr	Asp	Val	Met	Leu	Asn	Gln	Thr	Asn	Leu	Gln
154				100					105					110		
155	Phe	Asn	Asn	Asn	Lys	Tyr	Tyr	Leu	Ile	Gln	Leu	Leu	Glu	Asp	Asp	Ala
156			115					120					125			
157	Gln	Arg	Asn	Phe	Ser	Val	Trp	Met	Arg	Trp	Gly	Arg	Val	Gly	Lys	Met
158		130					135					140				
159	Gly	Gln	His	Ser	Leu	Val	Ala	Cys	Ser	Gly	Asn	Leu	Asn	Lys	Ala	Lys
160	145					150					155					160
161	Glu	Ile	Phe	Gln	Lys	Lys	Phe	Leu	Asp	Lys	Thr	Lys	Asn	Asn	Trp	Glu
162					165					170					175	
163	Asp	Arg	Glu	Lys	Phe	Glu	Lys	Val	Pro	Gly	Lys	Tyr	Asp	Met	Leu	Gln
164				180					185					190		
165	Met	Asp	Tyr	Ala	Thr	Asn	Thr	Gln	Asp	Glu	Glu	Glu	Thr	Lys	Lys	Glu
166			195					200					205			
167	Glu	Ser	Leu	Lys	Ser	Pro	Leu	Lys	Pro	Glu	Ser	Gln	Leu	Asp	Leu	Arg
168		210					215					220				
169	Val	Gln	Glu	Leu	Ile	Lys	Leu	Ile	Cys	Asn	Val	Gln	Ala	Met	Glu	Glu
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171	Met	Met	Met	Glu	Met	Lys	Tyr	Asn	Thr	Lys	Lys	Ala	Pro	Leu	Gly	Lys
172					245					250					255	
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176			275					280					285			
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180	305					310					315					320
181	Leu	Glu	Ala	Leu	Gly	Asp	Ile	Glu	Ile	Ala	Ile	Lys	Leu	Val	Lys	Thr
182					325					330					335	
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Input Set : N:\Crf4\11132002\I701586C.raw

Output Set: N:\CRF4\11192002\I701586C.raw

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193   Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile
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195   Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile
196               435                      440                      445
197   Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser
198               450                      455                      460
199   Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu Gly
200   465                      470                      475                      480
201   Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu
202               485                      490                      495
203   Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser
204               500                      505                      510
205   Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala
206               515                      520                      525
207   Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn
208               530                      535                      540
209   Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu
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212               565                      570
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215 <211> LENGTH: 2265
216 <212> TYPE: DNA
217 <213> ORGANISM: Homo sapiens
218 <220> FEATURE:
219 <221> NAME/KEY: CDS
220 <222> LOCATION: (242)...(1843)
221 <223> OTHER INFORMATION: product is Poly ADP Ribose Polymerase; from uterus tissue
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225   tctccctaata tcacgcctga ggctcatgga gagttgctag acctgggact gccctgggag      180
226   gcgcacacaa ccaggccggg tggcagccag gacctctccc atgtccctgc ttttcttggc      240
227   c atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct gag      286
228   Met Ala Pro Lys Lys Pro Trp Val Gln Thr Glu Gly Pro Glu
229   1          5          10          15
230   aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc tcc      334
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232               20          25          30
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234   Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg
235               35          40          45
236   gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg tat      430
237   Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr
238               50          55          60
239   gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac aac      478
240   Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn
241               65          70          75
242   aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc ttc      526

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Input Set : N:\Crf4\11132002\I701586C.raw
 Output Set: N:\CRF4\11192002\I701586C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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 Seq#:13; Xaa Pos. 33,41,42,43,48
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 Seq#:15; Xaa Pos. 29,30,31,32
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 Seq#:29; Xaa Pos. 2,3,4
 Seq#:30; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 23
 Seq#:3; Line(s) 221
 Seq#:5; Line(s) 418
 Seq#:11; Line(s) 988
 Seq#:13; Line(s) 1034,1035
 Seq#:15; Line(s) 1082
 Seq#:16; Line(s) 1099
 Seq#:17; Line(s) 1115
 Seq#:21; Line(s) 1180,1181
 Seq#:30; Line(s) 1297

VERIFICATION SUMMARY

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Input Set : N:\Crf4\11132002\I701586C.raw

Output Set: N:\CRF4\11192002\I701586C.raw

L:9 M:270 C: Current Application Number differs, Wrong Format

L:994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0

L:1017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0

L:1019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:16

L:1041 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0

L:1043 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:16

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